Electronic Supplementary Material (ESI) for Biomaterials Science.

Supporting Information

A Simple and Programmable Dual-mode Aptasensor for Ultrasensitive Detection of Multidrug-resistant bacteria

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Table S1. The sequences of the aptamers used in this work.

Name	Sequence (5'→3')
MRSA aptamer 1 [1]	NH_2-CCATCCACACTCCGCAAGGGTGCCCCGGGGGGCTGTTCAGCGTGGTGGTGGGATGCCGTTTTGGTCCTTAGTCTCCGTCGTCGGCTGCCTCTACAT
MRSA aptamer 2	SH-CCATCCACACTCCGCAAGGGTGCCCCGGGGGGCTGTTCAGCGTGGTGGTGGGATGCCGTTTTGGTCCTTAGTCTCCGTCGTCGGCTGCCTCTACAT-BHQ2
MRSA probe	TTTTTTATGTAGAGGCAG-Cy5
E. coli aptamer 1[2]	NH_2-GGCAGGACACCGTAACGGGTATGCAGCTATCCCGGGCGCTGTCTGAAGATCGTGTGCTGCT
E. coli aptamer 2	SH-GGCAGGACACCGTAACGGGTATGCAGCTATCCCGGGCGCTGTCTGAAGATCGTGTGCTGCT-BHQ2
E. coli probe	TTTTTTAGCAGCACACGA -Cy5
M. tuberculosis aptamer 1[3]	NH_2-GGTGTGTTGACTGAGGGGGTGGGGTGGGTGGTGGTGGATATAGC
M. tuberculosis aptamer 2	SH-GGTGTGTTGACTGAGGGGGTGGGGTGGGTGGTGGTGGATATAGC-BHQ2
M. tuberculosis probe	TTTTTTGCTATATCCACC-Cy5
A.baumanii aptamer 1 [4]	NH_2-TACATGGTCAACCAAATTCTTGCAAATTCTGCATTCCTACTGT
A.baumanii aptamer 2	SH-TACATGGTCAACCAAATTCTTGCAAATTCTGCATTCCTACTGT-BHQ2
A.baumanii probe	TTTTTTACAGTAGGAATG-Cy5
P. aeruginosa aptamer 1[5]	NH_2-GCGCGCGAGATTAACCCCCCAATGCTGCACCGAGCCACGA
P. aeruginosa aptamer 2	SH-GCGCGCGAGATTAACCCCCCAATGCTGCACCGAGCCACGA-BHQ2
P. aeruginosa probe	TTTTTTTCGTGGCTCGGT -Cy5

The highlighted fragment by the yellow background is the binding region of the probe to the aptamer.

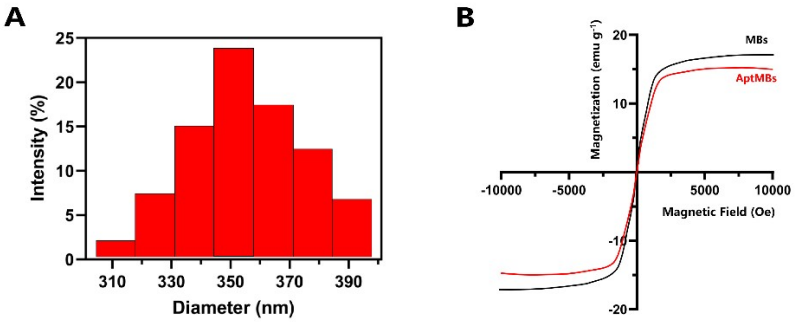

Fig. S1. (A) Size distribution histograms of MBs and (B) Magnetic hysteresis loop of MBs and AptMBs.

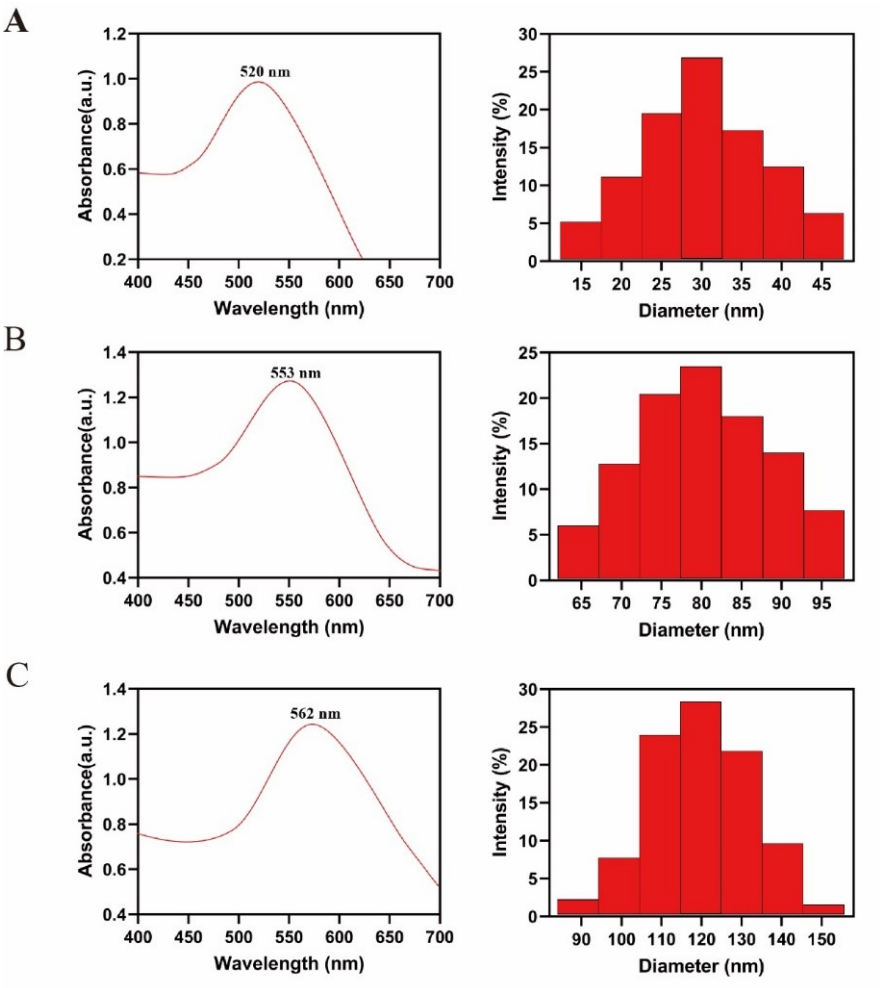

Fig. S2. Characterization of the synthesized GNPs with sizes of 30, 80, and 120 nm through UV−vis absorption spectra.

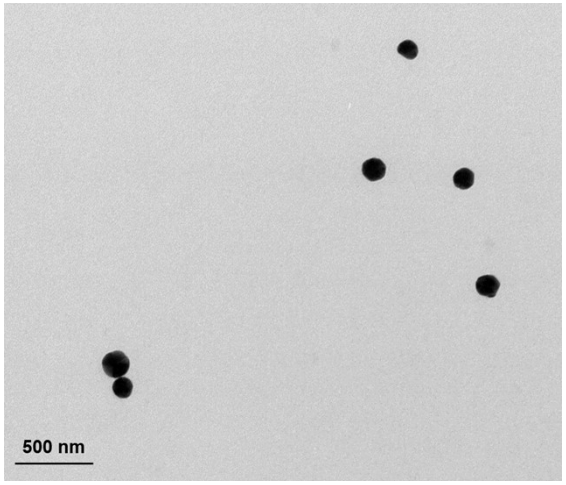

Fig S3. TEM image of AptGNPs (scale bar: 500 nm)

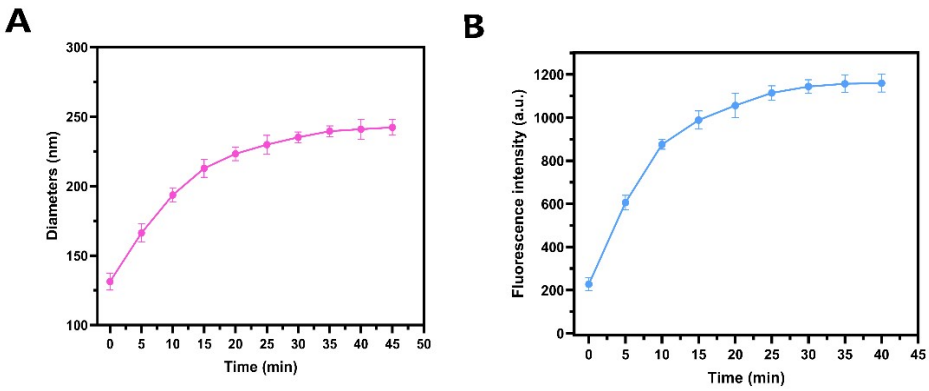

Fig. S4. Recognition time of AptGNPs on dual-mode: (A) Mode-DLS and (B) Mode-Flu.

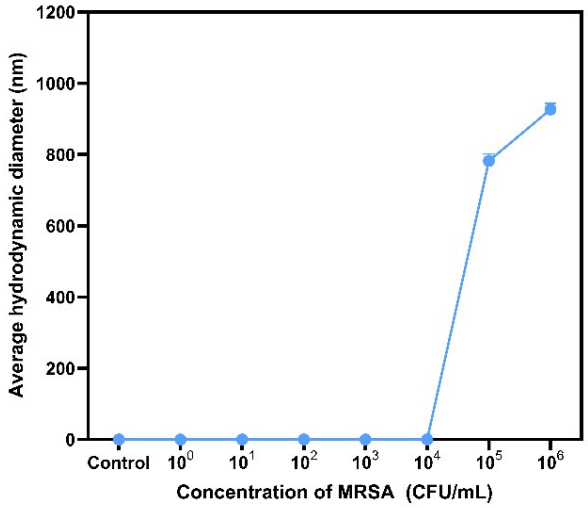

Fig. S5. The average D_H of MRSA.

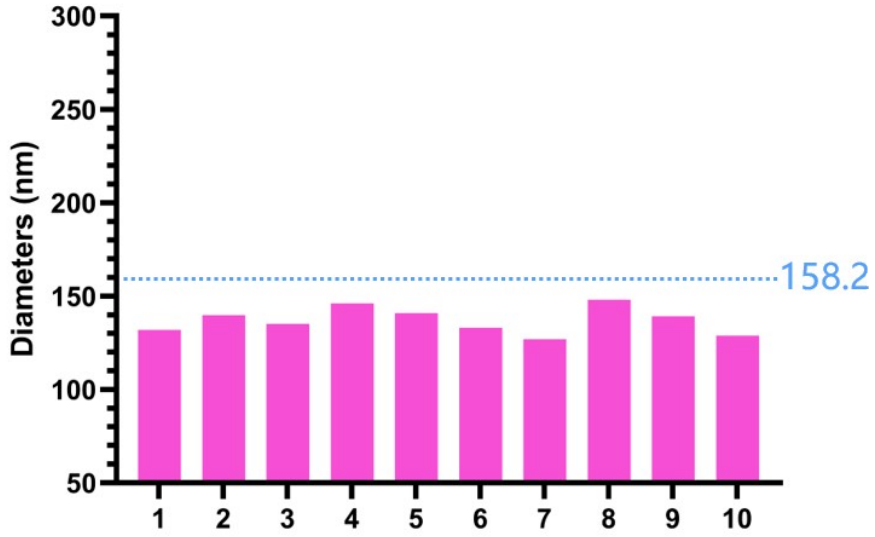

Fig. S6. The hydrodynamic diameter among 10 independent replications in the absence of MRSA. The threshold value of fluorescence intensity was defined as the mean value of negative samples plus 3 standard derivations.

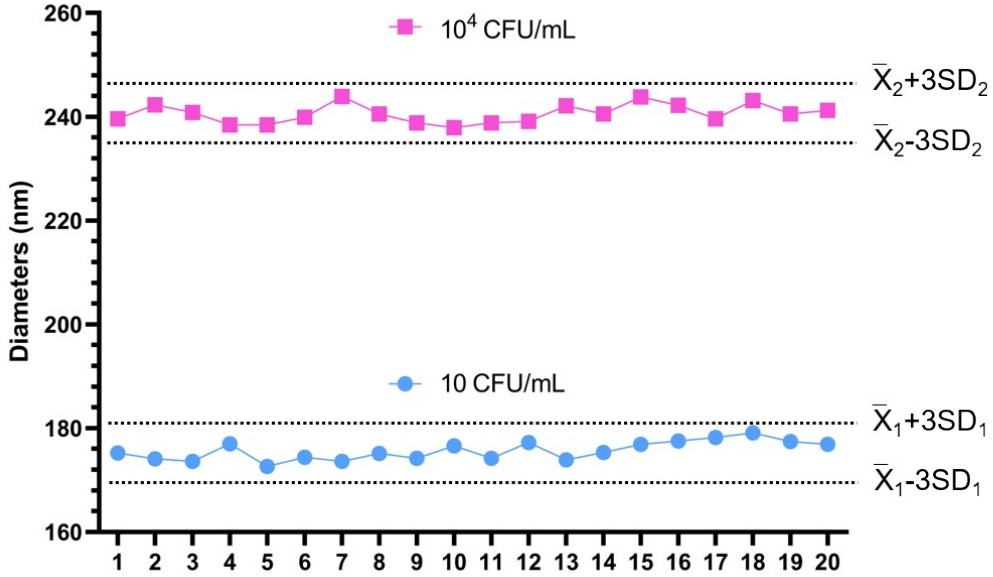

Fig. S7. Levey-Jennings chart-based control for 10 CFU/mL and 10^4 CFU/mL of MRSA concentrations detected by Mode-DLS. $\bar{X}_1$ and $\bar{X}_2$ represent the mean D_H of 10 CFU/mL and 10^4 CFU/mL, and their corresponding standard deviation is SD_1 and SD_2, respectively.

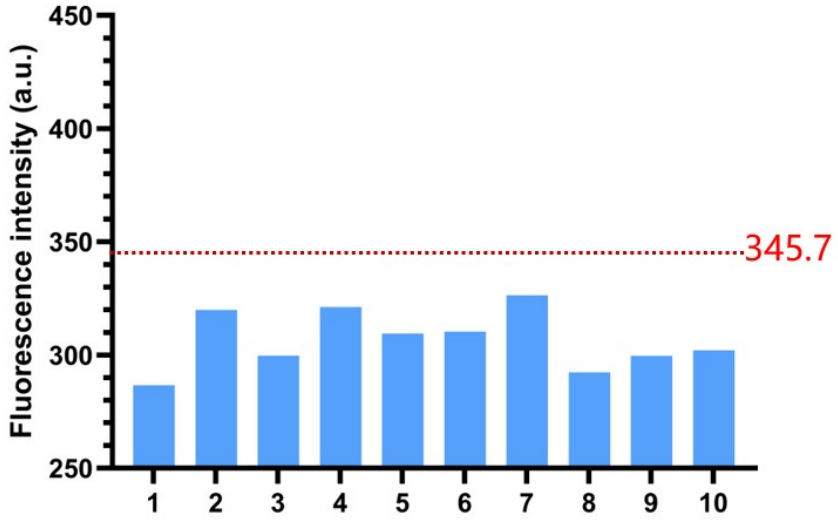

Fig. S8. The peak fluorescence intensity among 10 independent replications in the absence of MRSA. The threshold value of fluorescence intensity was defined as the mean value of negative samples plus 3 standard derivations.

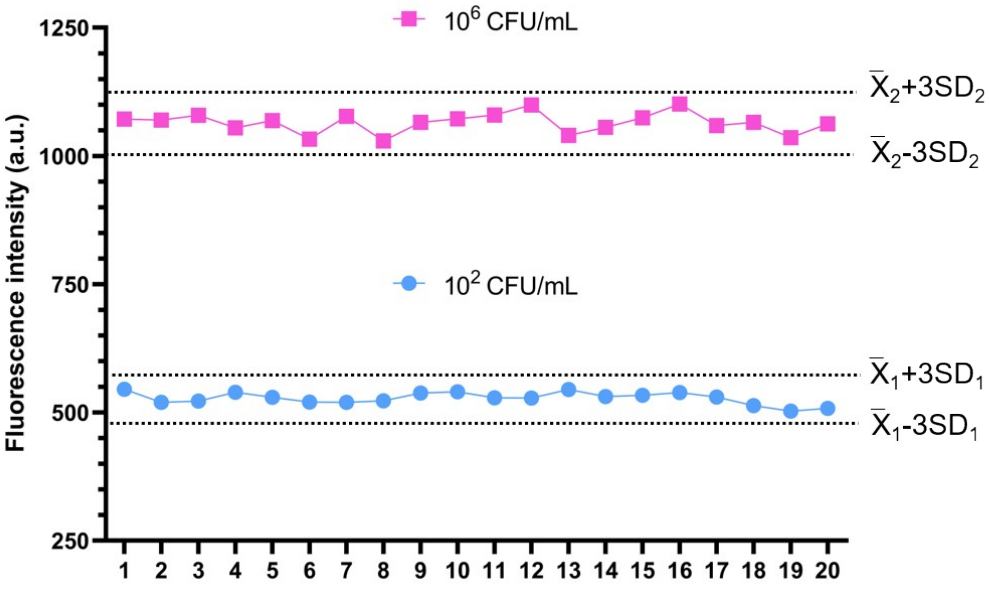

Fig. S9. Levey-Jennings chart-based control for 10^2 CFU/mL and 10^6 CFU/mL of MRSA concentrations detected by Mode-Flu. $\overline{X}_1$ and $\overline{X}_2$ represent the mean fluorescence intensity of 10^2 CFU/mL and 10^6 CFU/mL, and their corresponding standard deviation is SD_1 and SD_2, respectively.

Table S2. Summary of the proposed methods for MDR bacteria detection.

Method	Target	Platform	LOD (CFU/mL)	Detection time (min)	Ref.
EXPAR	MDR bacteria	Yes	6.73	70	[6]
RPA and Cas12a	Drug-resistant *Salmonella*	No	1	40	[7]
Multiplex PCR and CRISPR-Cas system	Drug-resistant *A. Baumannii*	No	50	120	[8]
Fluorescent microspheres	MRSA	No	110	10	[9]
Modified RPA	Drug-resistant *E. coli*	No	319	60	[10]
Blue polymeric nanobeads	MRSA	No	2	5	[11]
/	MRSA	No	845	270	[12]
DAPT	MDR bacteria	Yes	4.63	60	This work

References

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